PTO-1542
(4-85)

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4 DISKS

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****

USER Fredman SERIAL NUMBER 08/327,522

ART UNIT 1807 PHONE 308-6568 DATE _____

Please give a detailed statement of requirements. Describe as specifically as possible the subject matter to be searched. Define any terms that may have special meaning. Give examples or relevant citations, authors, or keywords, if known.

You may include a copy of the broadest and or relevant claim(s).

Please Search the following:

(1) Seq ID# Nos: 1-13 in Normal and prodigy disk

Limit hits to 5 for each search } please search complement please put on Disk

(2) Authors
- (a) David J. Lockhart
- (b) Mark S. Chee

(3) Search terms
- (a) array or biochip or library
- (b) hybridiz? or anneal?
- (c) Sequencing
- (d) RNAse A or enzym? or endonuclease or nuclease

if necessary

Thank you,

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SEARCHER Beverly @ 4999
ONLINE TIME 95/39 TOTAL TIME 105/54
(in minutes)
NO. OF DATABASES 2/1

SYSTEMS
- ✓ CAS ONLINE
- ___ DARC/QUESTEL
- ___ DIALOG
- ___ SDC
- ~~OTHER~~ IG

Acq: 7-217
Last: 7-218

Fredman
327522

```
=> fil reg; s tcggatcgactt | aacgcgccgcnc | cgcaacgcaagcgcggcgcg |
aacgcgcattcn | aaatataattcn | gatgcagcttccggaatgcgcg |
gatgcagcttccggaattatat | cgcgnnnnnn | cgcgcattcc |
aaagaaaaaagacagtactaaatgga | ttttttntgtcatga | tttttcngtcatgat |
ttttcgntcatgatt/sqsp
FILE 'REGISTRY' ENTERED AT 11:10:14 ON 27 JUL 95
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STRUCTURE FILE UPDATES:  21 JUL 95   HIGHEST RN 165171-57-3
DICTIONARY FILE UPDATES: 26 JUL 95   HIGHEST RN 165171-57-3

TSCA INFORMATION NOW CURRENT THROUGH JANUARY 1995

  Please note that search-term pricing does apply when
  conducting SmartSELECT searches.
```

Seq. IDs

```
L1             0 TCGGATCGACTT|AACGCGCCGCNC|CGCAACGCAAGCGCGGCGCG|AACGCGCATTC
                 N|AAATATAATTCN|GATGCAGCTTCCGGAATGCGCG|GATGCAGCTTCCGGAATTAT
                 AT|CGCGNNNNNN|CGCGCATTCC|AAAGAAAAAAGACAGTACTAAATGGA|TTTTTT
                 NTGTCATGA|TTTTTCNGTCATGAT|TTTTCGNTCATGATT/SQSP

=> fil ca; e lockhart d/au
FILE 'CA' ENTERED AT 11:10:37 ON 27 JUL 95
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FILE COVERS 1967 - 22 Jul 1995 (950722/ED)  VOL 123 ISS 4

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>>> Hit RNs and chemical structures now available with new <<<
>>> HITSTR format.                                          <<<


E1             1      LOCKHART CAMPBELL MACRAE/AU
E2             2      LOCKHART CRAIG H/AU
E3             1 --> LOCKHART D/AU
E4             1      LOCKHART D J/AU
E5             2      LOCKHART D R/AU
E6             1      LOCKHART DAVID/AU
E7            20      LOCKHART DAVID J/AU
E8             1      LOCKHART DENNIS/AU
E9             1      LOCKHART E A/AU
E10            3      LOCKHART EARLE A/AU
E11            1      LOCKHART EDWARD RAY/AU
E12            2      LOCKHART EWART ROBIN/AU
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- Author(s)

```
=> s e3 or e4 or e6 or e7; e chee m/au
```

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             1 "LOCKHART D"/AU
             1 "LOCKHART D J"/AU
             1 "LOCKHART DAVID"/AU
            20 "LOCKHART DAVID J"/AU
L2          23 "LOCKHART D"/AU OR "LOCKHART D J"/AU OR "LOCKHART DAVID"/A
               U OR "LOCKHART DAVID J"/AU


E1           2     CHEE L C/AU
E2           2     CHEE L Y/AU
E3           2 --> CHEE M/AU
E4           3     CHEE M S/AU
E5           5     CHEE MANUEL/AU
E6           5     CHEE MARK/AU
E7           4     CHEE MARK S/AU
E8           1     CHEE MELISSA KIE LIN/AU
E9           3     CHEE MERK NA/AU
E10          2     CHEE N P/AU
E11          1     CHEE NGEE ONN/AU
E12          1     CHEE O K/AU

=> s e3 or e4 or e6 or e7; s l2 and l3; s (l2 or l3) and hybridi?
             2 "CHEE M"/AU
             3 "CHEE M S"/AU
             5 "CHEE MARK"/AU
             4 "CHEE MARK S"/AU
L3          14 "CHEE M"/AU OR "CHEE M S"/AU OR "CHEE MARK"/AU OR "CHEE MA
               RK S"/AU


L4           0 L2 AND L3


         62898 HYBRIDI?
L5           1 (L2 OR L3) AND HYBRIDI?

=> d .beverly; fil biosi; s lockhart d ?/au; s chee m ?/au

L5   ANSWER 1 OF 1  CA  COPYRIGHT 1995 ACS
AN   115:176648  CA
TI   Enzymic multiplex DNA sequencing
SO   Nucleic Acids Res. (1991), 19(12), 3301-5
     CODEN: NARHAD; ISSN: 0305-1048
AU   Chee, Mark
PY   1991
AB   The problem of reading DNA sequence films has been reformulated
     using an easily implemented, multiplex version of enzymic DNA
     sequencing.  By utilizing a uniquely tagged primer for each
     base-specific sequencing reaction, the four reactions can be pooled
     and electrophoresed in a single lane.  This approach has been
     previously proposed for use with fluorescently labeled probes, and
     is analogous to the principle used in four-dye fluorescence
     sequencing except that the signals are resolved following
```

electrophoresis. After transfer to a nylon membrane, images are obtained sep. for each of the four reactions by **hybridization** using oligonucleotide probes. The images can then be superimposed to reconstitute a complete sequence pattern. In this way the correction of gel distortion effects and accurate band registration are considerably simplified, as each of the four base-specific ladders require very similar corrections. The methods therefore provide the basis for a second generation of more accurate and reliable film reading programs, as well as being useful for conventional multiplex sequencing. Unlike the original multiplex protocol, the approach described is suitable for small projects, as multiple cloning vectors are not used. Although more than one vector can be utilized, only a library of fragments cloned into any single phage, phagemid or plasmid vector is actually required, together with a set of tagged oligonucleotide primers.

FILE 'BIOSIS' ENTERED AT 11:11:54 ON 27 JUL 95
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CAS REGISTRY NUMBERS AND CHEMICAL NAMES (CNs) PRESENT
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RECORDS LAST ADDED: 11 July 1995 (950711/ED)
CAS REGISTRY NUMBERS (R) LAST ADDED: 11 July 1995 (950711/UP)

As of December 31, 1993 the BIOSIS File will be updated weekly with information from both publications. SDIs will now be run weekly. For more information enter HELP UPDATE and HELP COST at an arrow prompt(=>).

L6 19 LOCKHART D ?/AU

L7 24 CHEE M ?/AU

=> s l6 and l7; s (l6 or l7) and hybridi?
L8 2 L6 AND L7

68886 HYBRIDI?
L9 2 (L6 OR L7) AND HYBRIDI?

=> s l8 or l9; fil medl; s l6; s l7
L10 2 L8 OR L9

FILE 'MEDLINE' ENTERED AT 11:15:01 ON 27 JUL 95

FILE LAST UPDATED: 20 JUL 1995 (950720/UP). FILE COVERS 1966 TO DATE.
+QLF/CT SHOWS YOU THE ALLOWABLE QUALIFIERS OF A TERM.

MEDLINE, CANCERLIT AND PDQ ERRONEOUSLY ANNOTATED CERTAIN ARTICLES AUTHORED OR CO-AUTHORED BY DR. BERNARD FISHER WITH THE PHRASE "SCIENTIFIC MISCONDUCT-DATA TO BE REANALYZED." ALL SUCH ANNOTATIONS HAVE BEEN REMOVED OR ARE BEING REMOVED. WE APOLOGIZE FOR ANY PROBLEMS OR CONCERNS THIS MAY HAVE CAUSED. USERS SHOULD DISREGARD THOSE PRIOR ANNOTATIONS.

L11 6 LOCKHART D ?/AU

L12 16 CHEE M ?/AU

=> s l11 and l12; s (l11 or l12) and hybridi?
L13 0 L11 AND L12

73399 HYBRIDI?
L14 0 (L11 OR L12) AND HYBRIDI?

=> fil biotechd; s l6; s l7
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L15 0 LOCKHART D ?/AU

L16 0 CHEE M ?/AU

=> fil embas; s l6; s l7
FILE 'EMBASE' ENTERED AT 11:15:45 ON 27 JUL 95
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FILE COVERS 1974 TO 18 Jul 1995 (950718/ED)

L17 3 LOCKHART D ?/AU

L18 14 CHEE M ?/AU

=> s l17 and l18; s (l17 or l18) and hybridi?
L19 0 L17 AND L18

48903 HYBRIDI?
L20 0 (L17 OR L18) AND HYBRIDI?

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=> fil wpids; s l6;s l7
FILE 'WPIDS' ENTERED AT 11:16:29 ON 27 JUL 95
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FILE LAST UPDATED: 21 JUL 95                <950721/UP>
>>>UPDATE WEEKS:
MOST RECENT DERWENT WEEK            9528    <199528/DW>
DERWENT WEEK FOR CHEMICAL CODING:   9517
DERWENT WEEK FOR POLYMER INDEXING:  9522
DERWENT WORLD PATENTS INDEX SUBSCRIBER FILE, COVERS 1963 TO DATE
>>> DERWENT POLYMER INDEXING THESAURUS AVAILABLE IN FIELD /PLE <<<
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      >>> TIMELINESS OF UPDATING IMPROVED - SEE NEWS <<<
>>>NOW AVAILABLE - NEW USER MANUAL GLOBAL PATENT SOURCES - SEE NEWS<<<


L21           2 LOCKHART D ?/AU


L22           0 CHEE M ?/AU

=> s l21 and hybridi?
          3734 HYBRIDI?
L23           0 L21 AND HYBRIDI?

=> fil biosi; d l10 1-2 .beverly1; fil ca; s (array? or biochip? or bio
chip? or librar?) and (hybridi? or anneal?)
FILE 'BIOSIS' ENTERED AT 11:17:24 ON 27 JUL 95
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CAS REGISTRY NUMBERS AND CHEMICAL NAMES (CNs) PRESENT
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RECORDS LAST ADDED: 11 July 1995 (950711/ED)
CAS REGISTRY NUMBERS (R) LAST ADDED: 11 July 1995 (950711/UP)

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more information enter HELP UPDATE and HELP COST at an arrow
prompt(=>).


L10  ANSWER 1 OF 2  BIOSIS  COPYRIGHT 1995 BIOSIS
AN  94:525744  BIOSIS
DN  97538744
TI  DNA sequencing by hybridization on high density probe
    arrays: Enzymatic enhancement and sequence reconstruction.
AU  Lockhart D J; Chee M S
CS  Affymetrix, Santa Clara, CA, USA
SO  44th Annual Meeting of the American Society of Human Genetics,
```

Montreal, Quebec, Canada, October 18-22, 1994. American Journal of Human Genetics 55 (3 SUPPL.). 1994. A264. ISSN: 0002-9297

L10 ANSWER 2 OF 2 BIOSIS COPYRIGHT 1995 BIOSIS
AN 94:524319 BIOSIS
DN 97537319
TI Sequencing mitochondrial DNA polymorphisms by **hybridization**
.
AU **Chee M S; Lockhart D J**; Hubbell E; Morris M S
CS Affymetrix, 3380 Central Expressway, Santa Clara, CA 95051, USA
SO 44th Annual Meeting of the American Society of Human Genetics, Montreal, Quebec, Canada, October 18-22, 1994. American Journal of Human Genetics 55 (3 SUPPL.). 1994. A24. ISSN: 0002-9297

FILE 'CA' ENTERED AT 11:17:33 ON 27 JUL 95
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>>> Hit RNs and chemical structures now available with new <<<
>>> HITSTR format. <<<

-key terms Applicant's file specified

```
         33883 ARRAY?
            50 BIOCHIP?
         23684 BIO
         22363 CHIP?
             6 BIO CHIP?
                 (BIO(W)CHIP?)
         25949 LIBRAR?
         62898 HYBRIDI?
        131200 ANNEAL?
L24       7665 (ARRAY? OR BIOCHIP? OR BIO CHIP? OR LIBRAR?) AND (HYBRIDI?
               OR ANNEAL?)

=> s l24 and sequenc?
        296948 SEQUENC?
L25       5863 L24 AND SEQUENC?

=> fil reg; e rnase a/cn 5
FILE 'REGISTRY' ENTERED AT 11:18:42 ON 27 JUL 95
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DICTIONARY FILE UPDATES: 26 JUL 95   HIGHEST RN 165171-57-3
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TSCA INFORMATION NOW CURRENT THROUGH JANUARY 1995

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E1            1     RNASE (REINDEER PANCREAS REDUCED)/CN
E2            1     RNASE (SPALAX LEUCODON PANCREAS)/CN
E3            0 --> RNASE A/CN
E4            1     RNASE A (IMPALA PANCREAS REDUCED)/CN
E5            1     RNASE A (MYCOPLASMA CAPRICOLUM CLONE P8SU GENE RNPA C5
                     SUBUNIT)/CN

=> s ("rnase a"? or endonuclease? or nuclease?)/cn
             7 "RNASE A"?/CN
            34 ENDONUCLEASE?/CN
          1466 NUCLEASE?/CN
L26       1467 ("RNASE A"? OR ENDONUCLEASE? OR NUCLEASE?)/CN

=> fil ca; s l25 and (l26 or (rnase or ribonuclease)(w)a or endonuclease#
or nuclease#)
FILE 'CA' ENTERED AT 11:20:11 ON 27 JUL 95
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  HCA File when using the FSEARCH command or when conducting
  SmartSELECT searches with large numbers of terms.

>>> Hit RNs and chemical structures now available with new <<<
>>> HITSTR format.                                         <<<


         23196 L26
         20833 RNASE
          6469 RIBONUCLEASE
       8789608 A
          2917 (RNASE OR RIBONUCLEASE)(W)A
         16750 ENDONUCLEASE#
         15647 NUCLEASE#
L27        400 L25 AND (L26 OR (RNASE OR RIBONUCLEASE)(W)A OR ENDONUCLEAS
               E# OR NUCLEASE#)

=> d his l27-l44; s l33 not l5

     (FILE 'CA' ENTERED AT 11:20:11 ON 27 JUL 95)
L27        400 S L25 AND (L26 OR (RNASE OR RIBONUCLEASE)(W)A OR ENDONUCL
L28       7464 S (ARRAY? OR BIOCHIP? OR BIO CHIP? OR LIBRAR?)(L)(HYBRIDI
L29        216 S L27 AND PROBE#
L30          0 S L29 AND (HIGH DENSITY OR HD)
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L31        1666 S (ARRAY? OR BIOCHIP? OR BIO CHIP? OR LIBRAR?)(10A)(HYBRI
L32         262 S L31(10A)SEQUENC?
L33           2 S L32(10A)(L26 OR (RNASE OR RIBONUCLEASE)(W)A OR ENDONUCL
L34        5363 S L28(L)SEQUENC?
L35         344 S L34(L)(L26 OR (RNASE OR RIBONUCLEASE)(W)A OR ENDONUCLEA
L36        4830 S SEQUENC?(5A)(ANNEAL? OR HYBRIDI?)
L37         727 S L28(L)L36
L38         129 S L37(L)(L26 OR ENZYME# OR (RNASE OR RIBONUCLEASE)(W)A OR
L39          64 S L38 AND PROBE#
L40           0 S L38(L)PROBE3
L41          63 S L38(L)PROBE#
L42        7804 S (ARRAY? OR BIOCHIP? OR BIO CHIP? OR LIBRAR?)(L)PROBE#
L43         362 S L36(L)L42
L44          63 S L43(L)(L26 OR ENZYME# OR (RNASE OR RIBONUCLEASE)(W)A OR


L46           2 L33 NOT L5

=> d 1-2

L46  ANSWER 1 OF 2  CA  COPYRIGHT 1995 ACS
AN   119:242307  CA
TI   Identification of two families of satellite-like repetitive DNA
     sequences from the zebrafish (Brachydanio rerio)
AU   Ekker, Marc; Fritz, Andreas; Westerfield, Monte
CS   Inst. Neurosci., Univ. Oregon, Eugene, OR, 97403, USA
SO   Genomics (1992), 13(4), 1169-73
     CODEN: GNMCEP; ISSN: 0888-7543
DT   Journal
LA   English

L46  ANSWER 2 OF 2  CA  COPYRIGHT 1995 ACS
AN   112:173298  CA
TI   Structure and expression of the murine slow/cardiac troponin C gene
AU   Parmacek, Michael S.; Leiden, Jeffrey M.
CS   Howard Hughes Med. Inst., Univ. Michigan, Ann Arbor, MI, 48109, USA
SO   J. Biol. Chem. (1989), 264(22), 13217-25
     CODEN: JBCHA3; ISSN: 0021-9258
DT   Journal
LA   English

=> d 1-2  .beverly

L46  ANSWER 1 OF 2  CA  COPYRIGHT 1995 ACS
AN   119:242307  CA
TI   Identification of two families of satellite-like repetitive DNA
     sequences from the zebrafish (Brachydanio rerio)
SO   Genomics (1992), 13(4), 1169-73
     CODEN: GNMCEP; ISSN: 0888-7543
AU   Ekker, Marc; Fritz, Andreas; Westerfield, Monte
PY   1992
AB   To further understanding of the structure and organization of the
     zebrafish genome, the authors have undertaken the anal. of highly
```

and middle-repetitive DNA sequences. They have cloned and sequenced two families of tandemly repeated DNA fragments. The monomer units of the Type I satellite-like sequence are 186 bp long, A+T-rich (65%), and exhibit a high degree of sequence conservation. The Type I satellite-like sequence constitutes 8% of the zebrafish genome, or approx. 8 .times. 105 copies per haploid genome. Southern anal. of genomic DNA, digested with several restriction **endonucleases**, shows a ladder of **hybridizing** bands, consistent with a tandem **array**, and suggests longer range periodic variations in the **sequence** of the tandem repeats. The Type II satellite has a monomer length of 165 bp, is also A+T-rich (68%), and constitutes 0.2% of the zebrafish genome (22,000 copies per haploid genome). Southern anal. reveals a complex pattern rather than a ladder of regularly spaced hybridizing bands.

L46 ANSWER 2 OF 2 CA COPYRIGHT 1995 ACS
AN 112:173298 CA
TI Structure and expression of the murine slow/cardiac troponin C gene
SO J. Biol. Chem. (1989), 264(22), 13217-25
CODEN: JBCHA3; ISSN: 0021-9258
AU Parmacek, Michael S.; Leiden, Jeffrey M.
PY 1989
AB Cardiac troponin C (cTnC) is the calcium-binding subunit of the myofibrillar thin filament that regulates excitation-contraction coupling in cardiac muscle. A novel polymerase chain reaction cloning procedure was used to isolate cDNA clones encoding murine cTnC. Murine tTnC is a 161-amino-acid polypeptide that has been highly conserved during evolution. Southern blot analyses demonstrated that the cTnC gene is a member of a multigene family. Northern blot analyses revealed that the cTnC gene is expressed in murine cardiac tissue and slow skeletal muscle (soleus), but is not expressed in fast skeletal muscle (extensor digitorum longus and anterior tibialis) or in neonatal or adult brain, kidney, lung, liver, or testis. In addn., whereas the cTnC gene is not expressed in murine C2C12 myoblasts, differentiation of these cells into myotubes resulted in a dramatic induction of cTnC gene expression. A full-length cTnC genomic clone was isolated from a murine genomic **library** by **hybridization** with a cTnC cDNA probe and structurally characterized by DNA **sequence**, primer extension, and S1 **nuclease** protection analyses. The cTnC gene is 3.4 kilobase pairs long and is composed of 6 exons. The introns do not divide the gene into functional domains. Anal. of the 5'-flanking region of the gene revealed the presence of a consensus TATA box 24 base pairs 5' of the transcription start site. Despite the finding that the gene is expressed only in cardiac and slow skeletal muscle, it lacks the previously described CArG and M-CAT transcriptional regulatory sequence motifs that are involved in regulating the expression of a no. of other myofibrillar genes.

=> d que
L26 1467 SEA FILE=REGISTRY ("RNASE A"? OR ENDONUCLEASE? OR NUCLEASE?)/CN
L47 964 SEA FILE=CA ARRAY? AND (HYBRIDI? OR ANNEAL?)

L48 93 SEA FILE=CA L47 AND (L26 OR ENZYME# OR (RNASE OR RIBONUCL EASE)(W)A OR ENDONUCLEASE# OR NUCLEASE#)
L49 71 SEA FILE=CA L48 AND SEQUENC?
L50 14 SEA FILE=CA L49 AND (LIBRAR? OR BIOCHIP? OR BIO CHIP?)

=> s l50 not l46
L51 14 L50 NOT L46

=> d 1-14 .beverly; fil biosi; s array?(1)(hybridi? or anneal?)

L51 ANSWER 1 OF 14 CA COPYRIGHT 1995 ACS
AN 121:273529 CA
TI Selection of cDNAs using chromosome-specific genomic clones: application to human chromosome 13
SO Hum. Mol. Genet. (1994), 3(9), 1663-1673
CODEN: HMGEE5; ISSN: 0964-6906
AU de Fatima Bonaldo, Maria; Yu, Ming-Tsung; Jelenc, Pierre; Brown, Stephen; Su, Long; Lawton, Lee; Deaven, Larry; Efstratiadis, Argiris; Warburton, Dorothy; Soares, Marcelo Bento
PY 1994
AB We have developed a general method for en masse isolation of cDNAs present in a normalized **library** by **hybridization** to **arrayed** chromosome-specific phage .lambda. clones; we have used this approach to initiate exon-mapping of human chromosome 13. An advantage of the simultaneous isolation of cDNA/.lambda. pairs is that it allows cytogenetic assignment of a bona fide genomic clone by in situ **hybridization**, which also verifies that the corresponding cDNA or a homologous expressed **sequence** resides on chromosome 13. This information is enriched by partial **sequencing** of a selected cDNA from both ends. The **sequence** of the 3' noncoding region provides an 'identifier' that is used to develop STSs, while the **sequence** from the 5' end, often corresponding to a coding region, is used for homol. searches in databases that occasionally reveal gene functions.

L51 ANSWER 2 OF 14 CA COPYRIGHT 1995 ACS
AN 119:218942 CA
TI A repetitive element in the genome of Atlantic salmon, Salmo salar
SO Gene (1993), 131(2), 237-42
CODEN: GENED6; ISSN: 0378-1119
AU Goodier, John L.; Davidson, William S.
PY 1993
AB When Atlantic salmon (Salmo salar) genomic DNA is digested with the restriction **endonuclease** Bg/I and the fragments sepd. by agarose-gel electrophoresis, bands corresponding to approx. 430 and 923 bp are visualized after EtdBr staining. The 923-bp band was excised from a preparative gel and used to screen a salmon genomic **library** for recombinant phage (re-phage) contg. the repeat. The BglI repeat element is tandemly **arrayed**, and an **array** from one re-phage has been **sequenced**. The BglI repeats comprise 2.3% of the S. salar genome and have been found in the vicinity of rDNA genes (encoding rRNA). Southern blot

hybridization detects a homolog of the Atlantic salmon BglI repeat in the brown trout (Salmo trutta) genome, but not in other salmonids. However, a DNA fragment with **sequence** homol. to part of the BglI repeat has recently been isolated from Arctic charr (Salvelinus alpinus; S.E. Hartley and W.S.D., unpublished data). In addn., the BglI repeat detects RFLPs in Atlantic salmon.

L51 ANSWER 3 OF 14 CA COPYRIGHT 1995 ACS
AN 118:250513 CA
TI Cloning of the gene encoding Leishmania donovani S-adenosylhomocysteine hydrolase, a potential target for antiparasitic chemotherapy
SO Mol. Biochem. Parasitol. (1992), 53(1-2), 169-83
CODEN: MBIPDP; ISSN: 0166-6851
AU Henderson, Debbie M.; Hanson, Sheri; Allen, Thomas; Wilson, Keith; Coulter-Karis, Donna E.; Greenberg, Michael L.; Hershfield, Michael S.; Ullman, Buddy
PY 1992
AB A full-length gene encoding S-adenosylhomocysteine hydrolase (AdoHcyase) has been isolated from a genomic **library** of L. donovani DNA in .lambda.GEM-11 by cross-**hybridization** to the full-length human AdoHcyase cDNA. The nucleotide **sequence** of the SalI fragment contained a single open reading frame that encoded a polypeptide of 438 amino acids (47,712 Da). After max. gap alignment, the predicted amino acid **sequence** of the leishmanial AdoHcyase was 70-73% identical to AdoHCyases from higher eukaryotes. In addn., a database search revealed that the primary structure of all AdoHcyase proteins was highly homologous to that of a protein encoded by mRNA from Drosophila melanogaster that maps near the r element function of the Abd-b homeotic gene. In Northern blots, the SalI fragment **hybridized** to a 3.0-kb transcript that presumably encodes the parasite **enzyme**. Southern blot anal. of genomic DNA revealed that the AdoHcyase gene did not exist as a tandemly repeated **array** within the L. donovani genome. Moreover, monoclonal antibodies generated against human AdoHcyase recognized a leishmanial protein on immunoblots. Finally, the growth of L. donovani promastigotes could be arrested by micromolar concns. of 3-deazaaristeromycin (C3Ari) and 9-(trans-2',trans-3'-dihydroxycyclopentanyl)adenine, 2 known inhibitors of mammalian AdoHcyase. C3Ari also induced a substantial expansion of the intracellular pools of both AdoHcy and S-adenosylmethionine (AdoMet), as well as a significant diminution of the AdoMet/AdoHcy ratio. Thus, AdoHcyase may have therapeutic potential for the selective treatment of diseases of parasitic origin.

L51 ANSWER 4 OF 14 CA COPYRIGHT 1995 ACS
AN 118:162238 CA
TI Syntenic conservation of HSP70 genes in cattle and humans
SO Genomics (1992), 14(4), 863-8
CODEN: GNMCEP; ISSN: 0888-7543
AU Grosz, Michael D.; Womack, James E.; Skow, Loren C.
PY 1992

AB A phage **library** of bovine genomic DNA was screened for **hybridization** with a human HSP70 cDNA probe, and 21 pos. plaques were identified and isolated. Restriction mapping and blot **hybridization** anal. of DNA from the recombinant plaques demonstrated that the cloned DNAs were derived from 3 different regions of the bovine genome. One region contains 2 tandemly **arrayed** HSP70 **sequences**, designated HSP70-1 and HSP70-2, sepd. by .apprx.8 kb of DNA. Single HSP70 **sequences**, designated HSP70-3 and HSP70-4, were found in 2 other genomic regions. Locus-specific probes of unique flanking **sequences** from representative HSP70 clones were **hybridized** to restriction **endonuclease**-digested DNA from bovine-hamster and bovine-mouse somatic cell hybrid panels to det. the chromosomal location of the HSP70 **sequences**. The probe for the tandemly **arrayed** HSP70-1 and HSP70-2 **sequences** mapped to bovine chromosome 23, syntenic with glyoxalase 1, 21-steroid hydroxylase, and major histocompatibility class I loci. HSP70-3 **sequences** mapped to bovine chromosome 10, syntenic with nucleoside phosphorylase and murine osteosarcoma viral oncogene (v-fos), and HSP70-4 mapped to bovine syntenic group U6, syntenic with amylase 1 and phosphoglucomutase 1. On the basis of these data, the authors propose that bovine HSP70-1,2 are homologous to human HSPA1 and HSPA1L on chromosome 6p21.3, bovine HSP70-3 is the homolog of an unnamed human HSP70 gene on chromosome 14q22-q24, and bovine HSP70-4 is homologous 14q22-q24, and bovine HSP70-4 is homologous to one of the human HSPA-6,-7 genes on chromosome 1.

L51 ANSWER 5 OF 14 CA COPYRIGHT 1995 ACS
AN 117:185886 CA
TI An STS from a cDNA located in the myotonic dystrophy region (DM) on human chromosome 19q13.3
SO Hum. Mol. Genet. (1992), 1(3), 217
CODEN: HMGEE5; ISSN: 0964-6906
AU Lennon, G. G.; Lamerdin, J.; Lieuallen, K.; Amemiya, C.; Aslanidis, C.; De Jong, P. J.; Carrano, A. V.
PY 1992
AB In order to isolate genes from the myotonic dystrophy (DM) region. The authors screened an **arrayed** cDNA **library** of 18,432 human fetal brain cDNA clones with radiolabeled cosmid DNA derived from cosmid subclones of a yeast artificial chromosome known to be from the DM region. Cosmid y100172 identified one partial cDNA (45H9) which was subsequently **sequenced**, and is from a previously unknown human gene. Primers for PCR were selected (45H9-4, 5'-CGTCCGTGTTCCATCCTC, and 45H9-5, 5'-TTGGCAAAAGCAAATTTCC), along with reaction conditions consisting of 30 cycles of 95.degree. for 1 min, 58.degree. for 2 min, and 72.degree. for 2 min. When performed on genomic and cloned DNA, this verified that the single PCR product is derived from the region encompassed by cosmid y100172 on chromosome 19q13.3, and is likely to be from within a single exon. A Southern blot of genomic DNA **hybridized** with the PCR product as probe showed that this PCR product is genomically unique, identifying single bands of approx. 9, 1, and >18 kb when

the **enzymes** EcoRI, BamHI, and XbaI, resp., are used, and two bands (due to an internal HindIII site present in the **sequenced** 139 bp) of 8 and 16 kb for HindIII-digested genomic DNA. This **sequence** tagged site (STS) has been assigned D-segment no. D19S201. EMBL accession no. X62402.

L51 ANSWER 6 OF 14 CA COPYRIGHT 1995 ACS
AN 117:2048 CA
TI Cosmid linking clones localized to the long arm of human chromosome 11
SO Genomics (1992), 13(1), 134-43
CODEN: GNMCEP; ISSN: 0888-7543
AU Hermanson, G. G.; Lichter, P.; Selleri, L.; Ward, D. C.; Evans, G. A.
PY 1992
AB Mol. probes that contain DNA flanking CpG-rich restriction sites are extremely valuable in the construction of phys. maps of chromosomes and in the identification of genes assocd. with hypomethylated HTF (HpaII tiny fragment) islands. A new approach is described to the isolation and characterization of linking clones in **arrayed** chromosome-specific cosmid **libraries** through the large-scale semiautomated restriction mapping of cosmid clones. A cosmid **library** representing human chromosome 11q12-11qter was utilized and automated restriction **enzyme** anal. carried out followed by regional localization to chromosome 11q using high-resoln. in situ suppression **hybridization**. Using this approach, 165 cosmid linking clones contg. one or more NotI, BssHII, SfiI, or SacII sites were identified among 960 chromosome-specific cosmids. Furthermore, this anal. allowed clones contg. a single site to be distinguished from those contg. clusters of two or more rare sites. This anal. demonstrated that more than 75% of cosmids contg. a rare restriction site also contained a second rare restriction site, suggesting a high degree of CpG-rich restriction site clustering. Thirty chromosome 11q-specific cosmids contg. rare CpG-rich restriction sites were regionally localized by high-resoln. fluorescence in situ suppression **hybridization**, demonstrating that all of the CpG-rich sites detected by this method were located in bands 11q13 and 11q23. In addn., the distribution of (CA)n repetitive **sequences** was detd. by **hybridization** of the **arrayed** cosmid **library** with oligonucleotide probes, confirming a random distribution of microsatellites among CpG-rich cosmid clones. This set of reagent cosmid clones will be useful for phys. linking of large restriction fragments detected by pulsed-field gel electrophoresis and will provide a new and highly efficient approach to the construction of a phys. map of human chromosome 11q.

L51 ANSWER 7 OF 14 CA COPYRIGHT 1995 ACS
AN 116:77386 CA
TI Identification and characterization of novel human endogenous retroviral **sequences** prefentially expressed in undifferentiated embryonal carcinoma cells
SO Nucleic Acids Res. (1991), 19(7), 1513-20

CODEN: NARHAD; ISSN: 0305-1048

AU La Mantia, Girolama; Maglione, Domenico; Pengue, Gina; Di Cristofano, Antonio; Simeone, Antonio; Lanfrancone, Luisa; Lania, Luigi

PY 1991

AB A novel endogenous retroviral **sequence** (ERV-9) has been isolated from a human embryonal carcinoma cDNA **library** by **hybridization** to a probe contg. a recently described human repetitive element. DNA **sequence** anal. of the 4kb cDNA insert (pHE.1) revealed the presence of ORFs potentially coding for putative retrovirus-related gag, pol, and env proteins. Northern blot and RNase protection expts. showed that RNA homologous to the pHE.1 insert is detected only in embryonal carcinoma cells as an 8 kb mRNA, and its expression is neg. regulated during retinoic acid induced differentiation of the human teratocarcinoma cell line NT2/D1. Using a pol specific probe, a genomic locus contg. the ERV-9 **sequences** was isolated. Characterization by restriction **enzyme** anal. and DNA **sequencing** allowed for definition of LTR-like **sequences**, that are composed of a complex **array** of subrepetitive elements. In addn. the ERV-9 LTR **sequences** are able to drive expression of a linked CAT gene in a cell specific manner as LTR promoter activity has been detected only in NT2/D1 cells.

L51 ANSWER 8 OF 14 CA COPYRIGHT 1995 ACS

AN 114:137057 CA

TI Isolation and characterization of a repetitive DNA element from the genome of the human filarial parasite, Brugia malayi

SO Mol. Biochem. Parasitol. (1990), 43(1), 39-49
CODEN: MBIPDP; ISSN: 0166-6851

AU Natarajan, Sundareshwaran; Werner, Craig; Cameron, Margaret; Rajan, Thiruchandurai V.

PY 1990

AB The genome of the human filarial parasite B. malayi contains at least two major repetitive DNA elements. One, referred to as the HhaI family, consists of 104-105 tandemly **arrayed** copies per haploid genome of a monomer of 322 base pairs and does not contain a cleavage site for the restriction **endonuclease** MboI. The authors constructed a **library** of MboI-digested genomic B. malayi DNA in BamHI-cut M13mp18, resulting in the exclusion of the HhaI repeat family from the **library**. **Hybridization** of this genomic **library** with nick-translated genomic DNA yielded several copies of a repeat family which was named the BmMboI family. From **sequence** anal. of more than 50 monomers, which differ from each other in **sequence** and length, the monomers were divided into several regions based on the level of **sequence** conservation. Southern blot analyses of B. malayi genomic DNA digested with a variety of restriction **endonucleases** and probed with the isolated repeat demonstrate multiple bands of varying sizes except with HindIII-cut DNA, where the repeat is found only in very high-mol.-wt. DNA.

L51 ANSWER 9 OF 14 CA COPYRIGHT 1995 ACS
AN 113:146387 CA
TI Genomic arrangement of repeated PS700 elements in the nematode Panagrellus silusiae
SO Genome (1990), 33(2), 164-9
CODEN: GENOE3; ISSN: 0831-2796
AU Retterath, M. A.; Pasternak, J. J.
PY 1990
AB When genomic DNA from the free-living nematode P. silusiae is digested with the restriction **endonuclease** BamHI and sepd. by electrophoresis, a band in the 700 base pair size range is evident after ethidium bromide staining. One of the 0.7-kilobase fragments (PS700-1) was characterized and found to be a member of a moderately repetitive DNA family. DNA **sequence** analyses of three independently isolated copies of the PS700 DNA family showed the same nucleotide **sequence** and >98 similarity to PS700-1. Four EMBL-4 phage clones were isolated from a Panagrellus genomic DNA **library** with PS700-1 as the probe and were analyzed by restriction **endonuclease** site mapping and Southern blot DNA **hybridization**. These clones contain 31 copies of the PS700 DNA family. In each case, the units are arranged in head-to-tail **arrays**. One of the EMBL-4 clones contains copies of a novel variant of the PS700 elements. The maintenance of both nucleotide **sequence** and restriction **endonuclease** restriction site homogeneity among members of the dispersed PS700 DNA family may denote a functional role for these **sequences**.

L51 ANSWER 10 OF 14 CA COPYRIGHT 1995 ACS
AN 113:92260 CA
TI Structure and transcription of a human gene for H1 RNA, the RNA component of human RNase P
SO Nucleic Acids Res. (1990), 18(1), 97-103
CODEN: NARHAD; ISSN: 0305-1048
AU Baer, Madeline; Nilsen, Timothy W.; Costigan, Christine; Altman, Sidney
PY 1990
AB The gene coding for H1 RNA, the RNA component of human RNAse P, has been isolated and characterized from a human genomic DNA **library**. The **sequence** corresponding to the mature H1 RNA is almost identical to that previously identified using H1 RNA and a cDNA clone corresponding to it. The nucleotide **sequence** of the genomic clone contains an **array** of potential transcriptional control elements, some characteristic of transcription by RNA polymerase III and some characteristic of RNA polymerase II, as is also the case for U6 and certain other small stable RNAs. The transcription in vitro of the genomic clone shows that the gene is functional and is transcribed by RNA polymerase III. Southern **hybridization** anal. indicates that there is very likely only 1 copy of the gene for H1 RNA in the human genome.

L51 ANSWER 11 OF 14 CA COPYRIGHT 1995 ACS
AN 100:62781 CA

TI Isolation of DNA **sequences** preferentially expressed during sporulation in Saccharomyces cerevisiae
SO Mol. Cell. Biol. (1984), 4(1), 142-50
CODEN: MCEBD4; ISSN: 0270-7306
AU Percival-Smith, Anthony; Segall, Jacqueline
PY 1984
AB A differential **hybridization** screen was used to identify genes cloned from S. cerevisiae that are expressed preferentially during sporulation. Duplicate copies of a partial Sau3A yeast DNA **library** prepd. in the plasmid vector pBR322 were **hybridized** with radioactive cDNA probes representing the mRNA populations of sporulating a.alpha. cells and asporogenous .alpha..alpha. cells at various times after transfer to sporulation medium. Thirty-eight clones showed an enhanced **hybridization** signal with the a.alpha. sporulation probe relative to the .alpha..alpha. control cDNA probe. A comparison of the **array** of fragments produced by restriction **endonuclease** digestion of these plasmids suggested that 15 different **sequences** had been cloned. An RNA blot anal. using these cloned DNAs to probe RNAs purified from aa, a.alpha., and .alpha..alpha. cells harvested either during vegetative growth or at 10 h after transfer to sporulation medium indicated that 14 different sporulation-specific genes had been identified. Transcripts complementary to these genes are present only in a.alpha. cells after transfer to sporulation medium. Three of these clones contain 2 sporulation-specific genes. Three genes were identified that are expressed in all cell types during vegetative growth and only in a.alpha. cells in sporulation medium.

L51 ANSWER 12 OF 14 CA COPYRIGHT 1995 ACS
AN 99:117059 CA
TI Genomic organization, DNA **sequence**, and expression of chicken embryonic histone genes
SO J. Biol. Chem. (1983), 258(14), 9005-16
CODEN: JBCHA3; ISSN: 0021-9258
AU Sugarman, Barry J.; Dodgson, Jerry B.; Engel, James Douglas
PY 1983
AB Fifteen .lambda. Charon 4A recombinant bacteriophage contg. histone genes were isolated from a chicken genomic **library** and characterized in detail. Restriction **enzyme**-mapping anal. and Southern **hybridization** to **sequenced**, homologous histone probes indicate that these genes are not tandemly reiterated within the chicken genome; they usually reside in clusters, even though there is no unique **array** of genes that appears to constitute a typical cluster. Chicken H4 and H1 genes were identified within the genomic recombinants and subsequently **sequenced**. Extensive regions of homol. exist in the 5'- and 3'-flanking regions of the chicken H4 gene with H4 genes from other organisms. In addn. to the well documented histone-specific domains, 2 previously unreported regions of homol. lie 5' to this gene: an octanucleotide and a pentanucleotide **sequence** lying 59 and 116 nucleotides upstream from the H4 gene CAP site, resp. The H1 gene **sequence** predicts that

the H1 polypeptide is of 217 amino acids. The 5'-flanking domain of this gene contains, in addn. to the transcriptional initiation site and the ATA box, 2 unusual **sequences**; 1 is a nonamer which resides 29 nucleotides upstream from the ATA box and is conserved in both the chicken and sea urchin H1 genes, whereas the other is a (guanine + cytosine)-rich repetitive **sequence** element. The majority of the chicken histone genes among the 15 unique .lambda. recombinant clones are expressed almost exclusively during in ovo development (i.e. from .gtoreq.4 days postfertilization up to hatching, at .apprx.20-21 days postfertilization) and appear not to be assocd. with any particular tissue type.

L51 ANSWER 13 OF 14 CA COPYRIGHT 1995 ACS
AN 98:102055 CA
TI Molecular cloning of cDNA **sequences** for avian malic **enzyme**. Nutritional and hormonal regulation of malic **enzyme** mRNA levels in avian liver cells in vivo and in culture
SO J. Biol. Chem. (1983), 258(2), 1337-42
CODEN: JBCHA3; ISSN: 0021-9258
AU Winberry, Larry K.; Morris, Sidney M., Jr.; Fisch, Judith E.; Glynias, Manuel J.; Jenik, Robert A.; Goodridge, Alan G.
PY 1983
AB A double-stranded cDNA **library** constructed from the total poly(A+) RNA of goose uropygial gland was screened for recombinants contg. **sequences** complementary to malic **enzyme** (I) [9028-47-1] mRNA. Replicate **arrays** of 1400 colonies were **hybridized** independently with 32P-labeled cDNAs copied from 2 populations of hepatic RNA derived from tissues which differed by .apprx.35-fold with respect to the relative synthesis of I. Of the colonies which gave differential signals, 48 were further screened by hybrid-selected translation. DNA from 1 of these contained an insert of 970 base pairs and selected an mRNA which directed I synthesis in a cell-free system. The I **sequences** were subcloned into the single-stranded bacteriophage M13mp8. The subclones were used to prep. 32P-labeled single-stranded **hybridization** probes. Northern anal. indicated that I mRNA from both goose and chicken is .apprx.2100 bases in length. Hepatic I mRNA concn. is stimulated .gtoreq.30-50-fold when neonatal chicks or goslings, resp., are fed for 24 h. When added to chicken embryo hepatocytes in culture, triiodothyronine [6893-02-3] stimulated I mRNA accumulation by >100-fold. glucagon [9007-92-5] Inhibited the thyroid hormone-stimulated accumulation of I mRNA by 99%. In all instances, I mRNA concn. was closely correlated with the relative rate of I synthesis. Apparently, nutritional and hormonal regulation of I synthesis occurs at the pretranslational level.

L51 ANSWER 14 OF 14 CA COPYRIGHT 1995 ACS
AN 98:102028 CA
TI Members of the KpnI family of long interspersed repeated **sequences** join and interrupt .alpha.-satellite in the monkey genome
SO Nucleic Acids Res. (1983), 11(2), 321-38

CODEN: NARHAD; ISSN: 0305-1048
AU Grimaldi, Giovanna; Singer, Maxine F.
PY 1983
AB Three different members of a family (KpnI family) of interspersed repeated DNA **sequences** were found linked to .alpha.-satellite **sequences** in cloned segments of the African green monkey genome. In 2 of these segments, the KpnI family member is >6 kilobase pairs, and 1 of them is flanked by .alpha.-satellite on both sides, which indicates that it was inserted into a satellite **array**. **Hybridizations** of subcloned portions of the family members to restriction **endonuclease** digests of monkey and human DNA and to a genomic **library** of African green monkey DNA indicate that (1) family members are interspersed in both the monkey and human genomes, (2) some family members include **sequences** in addn. to those in the 3 characterized, (3) some family members might contain only parts of the **sequences** characterized, and (4) whereas the overall organization of the family is similar in the human and monkey genomes, the majority of the family members in each of the 2 genomes are distinctly identified by the variant positions of certain restriction **endonuclease** sites. This last observation suggests that within each genome, there is a tendency to maintain particular versions of the **sequence**. Observations (2) and (3) suggest that the KpnI family is complex and includes a variety of subfamilies.

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CAS REGISTRY NUMBERS (R) LAST ADDED: 11 July 1995 (950711/UP)

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          68886 HYBRIDI?
           2077 ANNEAL?
L52          415 ARRAY?(L)(HYBRIDI? OR ANNEAL?)

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         254631 SEQUENC?
L53          266 L52(L)SEQUENC?

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or nuclease#)
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         16603 RNASE
          2974 RIBONUCLEASE
       4457406 A
         13405 ENDONUCLEASE#
         18633 NUCLEASE#
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               DONUCLEASE# OR NUCLEASE#)

=> d his l52-

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L53         266 S L52(L)SEQUENC?
L54          52 S L53(L)(L26 OR ENZYME# OR (RNASE OR RIBONUCLEASE)(W)A OR
L55          18 S L54 AND PROBE#
L56          10 S L54 AND (LIBRAR? OR BIOCHIP? OR BIO CHIP?)
L57          20 S L55 OR L56

=> s l57 not l10
L58          20 L57 NOT L10

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         11285 ARRAY?
         73399 HYBRIDI?
          1838 ANNEAL?
        303111 SEQUENC?
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         25143 LIBRAR?
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          1599 CHIP?
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                 (BIO(W)CHIP?)
L59         22 L54 AND (PROBE# OR LIBRAR? OR BIOCHIP? OR BIO CHIP?)

=> fil biotechds; s l59
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           540 ARRAY?
          9620 HYBRIDI?
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         57300 ENZYME#
            36 RNASE
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           962 NUCLEASE#
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         185116 SEQUENC?
           5451 L26
         568394 ENZYME#
           5183 RNASE
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               DONUCLEASE# OR NUCLEASE#)
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L61           12 L54 AND (PROBE# OR LIBRAR? OR BIOCHIP? OR BIO CHIP?)

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DERWENT WEEK FOR CHEMICAL CODING:     9517
DERWENT WEEK FOR POLYMER INDEXING:    9522
DERWENT WORLD PATENTS INDEX SUBSCRIBER FILE, COVERS 1963 TO DATE
>>> DERWENT POLYMER INDEXING THESAURUS AVAILABLE IN FIELD /PLE <<<
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>>>NOW AVAILABLE - NEW USER MANUAL GLOBAL PATENT SOURCES - SEE NEWS<<<


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          3734 HYBRIDI?
         27405 ANNEAL?
         95853 SEQUENC?
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             0 ENDONUCLEASE?/CN
             0 NUCLEASE?/CN
         35176 ENZYME#
           153 RNASE
           323 RIBONUCLEASE
        146868 A
           650 ENDONUCLEASE#
           437 NUCLEASE#
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               DONUCLEASE# OR NUCLEASE#)
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          8900 BIO
         68180 CHIP?
             4 BIO CHIP?
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L62 0 L54 AND (PROBE# OR LIBRAR? OR BIOCHIP? OR BIO CHIP?)

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PROCESSING COMPLETED FOR L59
PROCESSING COMPLETED FOR L60
PROCESSING COMPLETED FOR L61
L63 27 DUP REM L58 L59 L60 L61 (30 DUPLICATES REMOVED)

=> d 1-27 bib abs; fil hom

L63 ANSWER 1 OF 27 BIOSIS COPYRIGHT 1995 BIOSIS DUPLICATE 1
AN 93:499541 BIOSIS
DN BA96:123548
TI A REPETITIVE ELEMENT IN THE GENOME OF ATLANTIC SALMON SALMO-SALAR.
AU GOODIER J L; DAVIDSON W S
CS DEP. BIOCHEM., MEMORIAL UNIV. NEWFOUNDLAND, ST. JOHN'S, NEWFOUNDLAND A1B 3-9, CAN.
SO GENE (AMST) 131 (2). 1993. 237-242. CODEN: GENED6 ISSN: 0378-1119
LA English
AB When Atlantic salmon (Salmo salar) genomic DNA is digested with the restriction **endonuclease** BglI and the fragments separated by agarose-gel electrophoresis, bands corresponding to approximately 430 and 923 bp are visualized after EtdBr staining. The 923-bp band was excised from a preparative gel and used to screen a salmon genomic **library** for recombinant phage (re-phage) containing the repeat. The BglI repeat element is tandemly **arrayed**, and an **array** from one re-phage has been **sequenced** . The BglI repeats comprise 2.3% of the S. salar genome and have been found in the vicinity of rDNA genes (encoding ribosomal RNA). Southern blot **hybridization** detects a homologue of the Atlantic salmon BglI repeat in the brown trout (Salmo trutta) genome, but not in other salmonids. However, a DNA fragment with **sequence** homology to part of the BglI repeat has recently been isolated from Arctic charr (Salvelinus alpinus; S.E. Hartley and W.S.D., unpublished data). In addition, the BglI repeat detects RFLPs in Atlantic salmon.

L63 ANSWER 2 OF 27 BIOSIS COPYRIGHT 1995 BIOSIS DUPLICATE 2
AN 93:225022 BIOSIS
DN BA95:116197
TI A SIMPLE METHOD OF DETECTING AMPLIFIED DNA WITH IMMOBILIZED

PROBES ON MICROTITER WELLS.
AU KAWAI S; MAEKAWAJIRI S; YAMANE A
CS INST. BIOTECHNOLOGY RES., WAKUNAGA PHARMACEUTICAL CO. LTD., 1624 SHIMOKOTACHI, KODA-CHO, TAKATA-GUN, HIROSHIMA 729-64, JPN.
SO ANAL BIOCHEM 209 (1). 1993. 63-69. CODEN: ANBCA2 ISSN: 0003-2697
LA English
AB We have developed a simple **hybridization** method for the detection of specific DNA **sequences** amplified by polymerase chain reaction (PCR). This method is similar to an **enzyme** -linked immunosorbent assay (ELISA) format in that labeled PCR products at the 5' termini are **hybridized** with **probes** immobilized on a microtiter well and the bound PCR products are detected in a manner similar to that of an **enzyme** immunoassay (EIA). Two improvements have been made in immobilizing the **probe** to the microtiter wells, in terms of increasing both immobility and **hybridization** efficiency. One is that single-stranded (ss) DNA, without the complementary strand, is used. The other is that instead of a single copy, a tandem **array** of the **probe** is used for immobilization and **hybridization**. Using of ssDNA containing about a 60-repeat **array** of a relevant **sequence** as an immobilized **probe**, the sensitivity increased 10-fold over that of a single oligonucleotide unit. We also found that the **hybridization** conditions such as time, temperature, and solution composition could be simplified. Therefore this method is especially suited for handling of a large number of samples, for example detection of viruses, bacteria, and other pathogens, as well as most human genetic disorders.

L63 ANSWER 3 OF 27 BIOTECHDS COPYRIGHT 1995 DERWENT INFORMATION LTD
AN 94-05459 BIOTECHDS
TI A new strategy for YAC-based mapping of human X-chromosome; yeast artificial chromosome-based human genome mapping involving hybridization and use of a DNA **probe** array (conference abstract)
AU Chai J H; Lin Y F
CS Univ.Fudan
LO Human Genome Laboratory, Institute of Genetics, Fudan University, Shanghai 200433, China.
SO Genome Mapping and Sequencing; (1993) 41
CODEN: 9999S
DT Journal
LA English
AN 94-05459 BIOTECHDS
AB A single copy DNA **probe sequence** gene bank was constructed. A new method for ordering yeast artificial chromosomes (YACs) was based on **hybridization** of membrane and YACs. The membrane was **array** spotted with single copy DNA **probes** and the YACs were screened out from YAC gene banks using the DNA **probes**. The single copy DNA **probes** were isolated from a human X-chromosome-specific phage lambda-Charon-35 gene bank. The gene bank DNA was digested with restriction **endonucleases** BamHI and HindIII. DNA

fragments of 0.2-1.0 kb were selected by agarose gel electrophoresis and ligated to plasmid pUC18. The single copy **sequence** clones were identified by **hybridization** with total human genome DNA. 1075 Single copy DNA clones were obtained. The DNA clones were spotted onto a nylon membrane as an **array**. The YAC clones were selected by **hybridization** with localized DNA **probes** which were isolated from the human X-chromosome. The YAC contig could be constructed from the data from the **hybridization** signal. The YAC DNA was labeled with an Alu **sequence** as primer and **hybridized** with the membrane. 100 YACs were selected and some YAC contigs were constructed using this method. (0 ref)

L63 ANSWER 4 OF 27 MEDLINE
AN 92372011 MEDLINE
TI Identification of two families of satellite-like repetitive DNA sequences from the zebrafish (Brachydanio rerio).
AU Ekker M; Fritz A; Westerfield M
CS Institute of Neuroscience, University of Oregon, Eugene 97403.
NC HD22486 (NICHD)
SO Genomics, (1992 Aug) 13 (4) 1169-73.
Journal code: GEN. ISSN: 0888-7543.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-M89943; GENBANK-M89944; GENBANK-M93288; GENBANK-S99479; GENBANK-S99543; GENBANK-S99546; GENBANK-S99553; GENBANK-S99558; GENBANK-S99567; GENBANK-X61631
EM 9211
AB To further our understanding of the structure and organization of the zebrafish genome, we have undertaken the analysis of highly and middle-repetitive DNA **sequences**. We have cloned and **sequenced** two families of tandemly repeated DNA fragments. The monomer units of the Type I satellite-like **sequence** are 186 bp long, A+T-rich (65%), and exhibit a high degree of **sequence** conservation. The Type I satellite-like **sequence** constitutes 8% of the zebrafish genome, or approximately 8 x 10(5) copies per haploid genome. Southern analysis of genomic DNA, digested with several restriction **endonucleases**, shows a ladder of **hybridizing** bands, consistent with a tandem **array**, and suggests longer range periodic variations in the **sequence** of the tandem repeats. The Type II satellite has a monomer length of 165 bp, is also A+T-rich (68%), and constitutes 0.2% of the zebrafish genome (22,000 copies per haploid genome). Southern analysis reveals a complex pattern rather than a ladder of regularly spaced **hybridizing** bands.

L63 ANSWER 5 OF 27 BIOSIS COPYRIGHT 1995 BIOSIS DUPLICATE 3
AN 93:140919 BIOSIS
DN BA95:73719
TI SYNTENIC CONSERVATION OF HSP70 GENES IN CATTLE AND HUMANS.

AU GROSZ M D; WOMACK J E; SKOW L C
CS DEP. VET. ANATOMY PUBLIC HEALTH, TEXAS A AND M UNIV., COLLEGE STATION, TEX. 77843.
SO GENOMICS 14 (4). 1992. 863-868. CODEN: GNMCEP ISSN: 0888-7543
LA English
AB A phase **library** of bovine genomic DNA was screened for **hybridization** with a human HSP70 cDNA **probe**, and 21 positive plaques were identified and isolated. Restriction mapping and blot **hybridization** analysis of DNA from the recombinant plaques demonstrated that the cloned DNAs were derived from three different regions of the bovine genome. One region contains two tandemly **arrayed** HSP70 **sequences**, designated HSP70-1 and HSP70-2, separated by approximately 8 kb of DNA. Single HSP70 **sequences**, designated HSP70-3 and HSP70-4, were found in two other genomic regions. Locus-specific **probes** of unique flanking **sequences** from representative HSP70 clones were **hybridized** to restriction **endonuclease** -digested DNA from bovine-hamster and bovine-mouse somatic cell hybrid panels to determine the chromosomal location of the HSP70 **sequences**. The **probe** for the tandemly **arrayed** HSP70-1 and HSP70-2 **sequences** mapped to bovine chromosome 23, syntenic with glyoxalase 1, 21 steroid hydroxylase, and major histocompatibility class I loci. HSP70-3 **sequences** mapped to bovine chromosome 10, syntenic with nucleoside phosphorylase and murine osteosarcoma viral oncogene (v-fos), and HSP70-4 mapped to bovine syntenic group U6, syntenic with amylase 1 and phosphoglucomutase 1. On the basis of these data, we propose that bovine HSP70-1,2 are homologous to human HSPA1 and HSPA1L on chromosome 6p21.3, bovine HSP70-3 is the homolog of an unnamed human HSP70 gene on chromosome 14q22-q24, and bovine HSP70-4 is homologous to one of the human HSPA-6,-7 genes on chromosome 1.

L63 ANSWER 6 OF 27 BIOSIS COPYRIGHT 1995 BIOSIS DUPLICATE 4
AN 92:411031 BIOSIS
DN BA94:74231
TI CLONING OF THE GENE ENCODING LEISHMANIA-DONOVANI S ADENOSYLHOMOCYSTEINE HYDROLASE A POTENTIAL TARGET FOR ANTIPARASITIC CHEMOTHERAPY.
AU HENDERSON D M; HANSON S; ALLEN T; WILSON K; COULTER-KARIS D E; GREENBERG M L; HERSHFIELD M S; ULLMAN B
CS DEP. BIOCHEMISTRY AND MOLECULAR BIOL., OREGON HEALTH SCI. UNIV., PORTLAND, OREGON 97201-3098, USA.
SO MOL BIOCHEM PARASITOL 53 (1-2). 1992. 169-183. CODEN: MBIPDP ISSN: 0166-6851
LA English
AB A full-length gene encoding the S-adenosylhomocysteine hydrolase (AdoHcyase) **enzyme** has been isolated from a genomic **library** of Leishmania donovani DNA in .lambda.GEM-11 by cross-**hybridization** to the full-length human AdoHcyase cDNA. The nucleotide **sequence** of the SalI fragment contained a single open reading frame that encoded a polypeptide of 438 amino acids (47712 Da). After maximum gap alignment, the predicted amino acid **sequence** of the leishmanial AdoHcyase

was 70-73% identical to AdoHCyases from higher eukaryotes. In addition, a data base search revealed that the primary structure of all AdoHcyase proteins was highly homologous to that of a protein encoded by a mRNA from Drosophila melanogaster that maps near the r element function of Abd-b homeotic gene. In Northern blots, the SalI fragment **hybridized** to a 3.0-kb transcript that presumably encodes the parasite **enzyme**. Southern blot analysis of genomic DNA revealed that the AdoHcyase gene did not exist as a tandemly repeated **array** within the L. donovani genome. Moreover, monoclonal antibodies generated against human AdoHcyase recognized a leishmanial protein on immunoblots. Finally, the growth of L. donovani promastigotes could be arrested by micromolar concentrations of 3-deazaaristeromycin (C3Ari) and 9-(trans-2', trans-3'-dihydroxycyclopentanyl)adenine, 2 known inhibitors of mammalian AdoHcyase. C3 Ari also induced a substantial expansion of the intracellular pools of both AdoHcy and S-adenosylmethionine (AdoMet), as well as a significant diminution of the AdoMet/AdoHcy ratio. Thus, AdoHcyase may have therapeutic potential for the selective treatment of diseases of parasitic origin.

L63 ANSWER 7 OF 27 BIOSIS COPYRIGHT 1995 BIOSIS DUPLICATE 5
AN 92:303694 BIOSIS
DN BA94:16844
TI COSMID LINKING CLONES LOCALIZED TO THE LONG ARM OF HUMAN CHROMOSOME 11.
AU HERMANSON G G; LICHTER P; SELLERI L; WARD D C; EVANS G A
CS MOLECULAR GENETICS LAB., SALK INST. BIOLOGICAL STUDIES, LA JOLLA, CALIF. 92037.
SO GENOMICS 13 (1). 1992. 134-143. CODEN: GNMCEP ISSN: 0888-7543
LA English
AB Molecular **probes** that contain DNA flanking CpG-rich restriction sites are extremely valuable in the construction of physical maps of chromosomes and in the identification of genes associated with hypomethylated HTF (HpaII tiny fragment) islands. We describe a new approach to the isolation and characterization of linking clones in **arrayed** chromosome-specific cosmid **libraries** through the large-scale semiautomated restriction mapping of cosmid clones. We utilized a cosmid **library** representing human chromosome 11q12-11qter and carried out automated restriction **enzyme** analysis, followed by regional localization to chromosome 11q using high-resolution in situ suppression **hybridization**. Using this approach, 165 cosmid linking clones containing one or more NotI, BssHII, SfiI, or SacII sites were identified among 960 chromosome-specific cosmids. Furthermore, this analysis allowed clones containing a single site to be distinguished from those containing clusters of two or more rare sites. This analysis demonstrated that more than 75% of cosmids containing a rare restriction site also contained a second rare restriction site, suggesting a high degree of CpG-rich restriction site clustering. Thirty chromosome 11q-specific cosmids containing rare CpG-rich restriction sites were regionally localized by high-resolution fluorescence in situ suppression **hybridization**, demonstrating that all the CpG-rich sites

detected by this method were located in bands 11q13 and 11q23. In addition, the distribution of (CA)n repetitive **sequences** were determined by **hybridization** of the **arrayed** cosmid **library** with oligonucleotide **probes**, confirming a random distribution of microsatellites among CpG-rich cosmid clones. This set of reagent cosmid clones will be useful for physical linking of large restriction fragments detected by pulsed-field gel electrophoresis and will provide a new and highly efficient approach to the construction of a physical map of human chromosome 11q.

L63 ANSWER 8 OF 27 MEDLINE
AN 92020989 MEDLINE
TI Origin of human chromosome 2: an ancestral telomere-telomere fusion.
AU IJdo J W; Baldini A; Ward D C; Reeders S T; Wells R A
CS Howard Hughes Medical Institute, Yale University School of Medicine, New Haven, CT 06510.
SO Proc Natl Acad Sci U S A, (1991 Oct 15) 88 (20) 9051-5.
Journal code: PV3. ISSN: 0027-8424.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
OS GENBANK-M73018; GENBANK-X59397; GENBANK-S60062; GENBANK-S60067; GENBANK-S60069; GENBANK-S60071; GENBANK-S60073; GENBANK-S60076; GENBANK-S60079; GENBANK-S60081
EM 9201
AB We have identified two allelic genomic cosmids from human chromosome 2, c8.1 and c29B, each containing two inverted **arrays** of the vertebrate telomeric repeat in a head-to-head arrangement, 5'(TTAGGG)n-(CCCTAA)m3'. **Sequences** flanking this telomeric repeat are characteristic of present-day human pretelomeres. BAL-31 **nuclease** experiments with yeast artificial chromosome clones of human telomeres and fluorescence in situ **hybridization** reveal that **sequences** flanking these inverted repeats **hybridize** both to band 2q13 and to different, but overlapping, subsets of human chromosome ends. We conclude that the locus cloned in cosmids c8.1 and c29B is the relic of an ancient telomere-telomere fusion and marks the point at which two ancestral ape chromosomes fused to give rise to human chromosome 2.

L63 ANSWER 9 OF 27 BIOSIS COPYRIGHT 1995 BIOSIS DUPLICATE 6
AN 91:279531 BIOSIS
DN BA92:12146
TI IDENTIFICATION AND CHARACTERIZATION OF NOVEL HUMAN ENDOGENOUS RETROVIRAL SEQUENCES PREFERENTIALLY EXPRESSED IN UNDIFFERENTIATED EMBRYONAL CARCINOMA CELLS.
AU LA MANTIA G; MAGLIONE D; PENGUE G; DI CRISTOFANO A; SIMEONE A; LANFRANCONE L; LANIA L
CS DEP. GENETICS GEN. AND MOL. BIOL., UNIV. NAPLES, VIA MEZZOCANNONE 8, 80124 NAPLES, ITALY.
SO NUCLEIC ACIDS RES 19 (7). 1991. 1513-1520. CODEN: NARHAD ISSN: 0305-1048

LA English
AB A novel endogenous retroviral **sequence** (ERV-9) has been isolated from a human embryonal carcinoma cDNA **library** by **hybridization** to a **probe** containing a recently described human repetitive element. DNA **sequence** analysis of the 4kb cDNA insert (pHE.1) revealed the presence of ORFs potentially coding for putative retrovirus-related gag, pol and env proteins. Northern blot and RNase protection experiments showed that RNA homologous to the pHE.1 insert is detected only in embryonal carcinoma cells as a 8 kb mRNA, and its expression is negatively regulated during retinoic acid induced differentiation of the human teratocarcinoma cell line NT2/D1. Using a pol specific **probe** we have isolated a genomic locus containing the ERV-9 **sequences**. Characterization by restriction **enzyme** analysis and DNA **sequencing** allowed us to define LTR-like **sequences**, that are composed by a complex **array** of subrepetitive elements. In addition we show that ERV-9 LTR **sequences** are capable to drive expression of linked CAT gene in a cell specific manner as LTR promoter activity has been detected only in NT2/D1 cells.

L63 ANSWER 10 OF 27 BIOTECHDS COPYRIGHT 1995 DERWENT INFORMATION LTD
AN 90-13394 BIOTECHDS
TI Chromosome DNA amplification; using the polymerase chain reaction; DNA **probe** construction
PA Univ.Miami
PI WO 9008821 9 Aug 1990
AI WO 90-US434 31 Jan 1990
PRAI US 89-304423 31 Jan 1989
DT Patent
LA English
OS WPI: 90-260931 [34]
AN 90-13394 BIOTECHDS
AB Isolating a gene located in a cytologically definable chromosomal region comprises: (a) microdissecting a chromosomal DNA segment from a pre-determined chromosomal region; (b) digesting the DNA segment with site-specific restriction **enzymes** to obtain DNA fragments having 2 ends; (c) ligating a primer DNA duplex to each of the 2 ends to obtain a hybrid DNA duplex linked to 2 primer DNA duplexes, such that formation of tandem **arrays** of 3 or more primer DNA duplexes is excluded; (d) denaturing the hybrid DNA duplexes to obtain 2 hybrid DNA stands having 5' and 3' ends; (e) **annealing** a primer to the 3' end of each of the strands; (f) amplifying the hybrid DNA strands using the polymerase chain reaction; (g) preparing **hybridization** **probes** by labeling the amplified DNA; and (h) using the **probes** to identify cDNA or genomic DNA clones bearing genes located within the chromosomal region. The ligation step is carried out in the presence of phage T4 DNA-ligase. The amplified DNA from step (f) is cloned and fragments corresponding to essentially non-repetitive sub-**sequences** of the dissected DNA are identified and used to produce **hybridization**

probes. (31pp)

L63 ANSWER 11 OF 27 MEDLINE
AN 91005330 MEDLINE
TI Localization and polymorphism of a chromosome 12-specific alpha satellite DNA sequence.
AU Looijenga L H; Smit V T; Wessels J W; Mollevanger P; Oosterhuis J W; Cornelisse C J; Devilee P
CS Department of Pathology, University of Groningen, The Netherlands.
SO Cytogenet Cell Genet, (1990) 53 (4) 216-8.
Journal code: DXK. ISSN: 0301-0171.
CY Switzerland
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 9101
AB The isolation and localization of a chromosome 12-specific alpha satellite DNA **sequence**, p alpha 12H8, is described. This clone contains a complete copy of the 1.4-kb HindIII higher-order repeat present within the alpha satellite **array** on chromosome 12. The specificity of p alpha 12H8 was demonstrated by in situ **hybridization** and Southern blot analysis of a somatic cell hybrid mapping panel, both performed under high-stringency conditions. Polymorphic restriction patterns within the alpha satellite **array**, revealed by the use of the restriction **enzymes** BglII and EcoRV, were demonstrated to display Mendelian inheritance. These properties make p alpha 12H8 a valuable genetic marker for the centromeric region of chromosome 12.

L63 ANSWER 12 OF 27 BIOSIS COPYRIGHT 1995 BIOSIS DUPLICATE 7
AN 90:331265 BIOSIS
DN BA90:39284
TI GENOMIC ARRANGEMENT OF REPEATED PS700 ELEMENTS IN THE NEMATODE PANAGRELLUS-SILUSIAE.
AU RETTERATH M A; PASTERNAK J J
CS DEP. BIOL., UNIV. WATERLOO, WATERLOO, ONTARIO, N2L 3G1, CAN.
SO GENOME 33 (2). 1990. 164-169. CODEN: GENOE3 ISSN: 0831-2796
LA English
AB When genomic DNA from the free-living nematode Panagrellus silusiae is digested with the restriction **endonuclease** BamHI and separated by electrophoresis, a band in the 700 base pair size range is evident after ethidium bromide staining. One of the 0.7-kilobase fragments (PS700-1) was characterized and found to be a member of a moderately repetitive DNA family (T. Warren and J.J. Pasternak. 1988. Nucleic Acids Res. 16: 10,833 - 10,847). In the current study, DNA **sequence** analyses of three independently isolated copies of the PS700 DNA family showed the same nucleotide **sequence** and >98% similarity to PS700-1. Four EMBL-4 bacteriophage clones were isolated from a Panagrellus genomic DNA **library** with PS700-1 as the **probe** and were analyzed by restriction **endonuclease** site mapping and Southern blot DNA **hybridization**. These clones contain 31 copies of the PS700 DNA family. In each case, the units are arranged in head-to-tail

arrays. One of the EMBL-4 clones contains copies of a novel variant of the PS700 elements. The maintenance of both nucleotide **sequence** and restriction **endonuclease** restriction site homogeneity among members of the dispersed PS700 DNA family may denote a functional role for these **sequences**.

L63 ANSWER 13 OF 27 BIOSIS COPYRIGHT 1995 BIOSIS DUPLICATE 8
AN 91:27429 BIOSIS
DN BA91:16780
TI ISOLATION AND CHARACTERIZATION OF A REPETITIVE DNA ELEMENT FROM THE GENOME OF THE HUMAN FILARIAL PARASITE BRUGIA-MALAYI.
AU NATARAJAN S; WERNER C; CAMERON M; RAJAN T V
CS UNIV. CONNECTICUT HEALTH CENTER, 263 FARMINGTON AVE. L-1006, FARMINGTON, CONN. 06032, USA.
SO MOL BIOCHEM PARASITOL 43 (1). 1990. 39-50. CODEN: MBIPDP ISSN: 0166-6851
LA English
AB The genome of the human filarial parasite Brugia malayi contains at least two major repetitive DNA elements. One, referred to as the HhaI family, consists of 104-105 tandemly **arrayed** copies per haploid genome of a monomer of 322 base pairs and does not contain a cleavage site for the restriction endonclease MboI. We constructed a **library** of MboI-digested genomic B. malayi DNA in BamHI-Cut M13mp18 resulting in the exclusion of the HhaI repeat family from the **library**. **Hybridization** of this genomic **library** with nick-translated genomic DNA yielded several copies of a repeat family which we have named the BmMbol family. From **sequence** analysis of more than 50 monomers, which differ from each other in **sequence** and length, we have been able to divide the monomers into several regions based on the level of **sequence** conservation. Southern blot analyses of B. malayi genomic DNA digested with a variety of restriction **endonucleases** and **probed** with the isolated repeat demonstrate multiple bands of varying sizes except with HindIII-cut DNA, where the repeat is found only in very high-molecular-weight DNA.

L63 ANSWER 14 OF 27 MEDLINE
AN 89306588 MEDLINE
TI A second locus for the 5S multigene family in Secale L.: sequence divergence in two lineages of the family.
AU Reddy P; Appels R
CS School of Agriculture, University of Melbourne, Victoria, Australia.
SO Genome, (1989 Jun) 32 (3) 457-67.
Journal code: FNP. ISSN: 0831-2796.
CY Canada
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 8910
AB The 5S RNA genes in Secale sp. are arranged as tandem **arrays** of a 460- and 480-bp repeating **sequence**. These size classes were initially discovered by restriction

endonuclease analysis using BamHI and subsequently by DNA **sequencing** of cloned units. The length variation between short and long units originated from major deletion-insertion events in the noncoding spacer region of the 5S DNA repeat units. In situ **hybridization** with [3H]cRNA and biotin-labelled **probes** synthesized from both the short and long 5S DNA units of S. cereale localized the sites on chromosome 1R and a new site on a chromosome identified as 5R. We propose that the chromosome 1R locus, which has been mapped previously, be named 5SDna-R1 and the second locus, reported in the present paper, be referred to as 5SDna-R2. A preferential **hybridization** of a **probe** from the long unit to the 5SDna-R2 locus and of a **probe** from the short unit to the 5SDna-R1 locus is reported. The clustering of long units in the 5SDna-R2 locus was confirmed by restriction **endonuclease** digestion of DNA from rye chromosome 5R additions to wheat. Nucleotide **sequence** alignment of 5S DNA repeat units from a number of Secale species, using both phenetic and cladistic computer programmes, demonstrated that two clear lineages corresponding to the long and short units existed in this genus. The different Secale species could not be unambiguously differentiated using the 5S DNA **sequences**.

L63 ANSWER 15 OF 27 BIOSIS COPYRIGHT 1995 BIOSIS
AN 89:381214 BIOSIS
DN BA88:61804
TI A SECOND LOCUS FOR THE 5S MULTIGENE FAMILY IN SECALE L. SEQUENCE DIVERGENCE IN TWO LINEAGES OF THE FAMILY.
AU REDDY P; APPELS R
CS INQ. J. P. GUSTAFSON, RES. JOURNALS, NATL. RES., COUNCIL OF CANADA, OTTAWA, CANADA K1A 0R6.
SO GENOME 32 (3). 1989. 456-467. CODEN: GENOE3 ISSN: 0831-2796
LA English
AB The 5S RNA genes in Secale sp. are arranged as tandem **arrays** of a 460- and 480-bp repeating **sequence**. These size classes were initially discovered by restriction **endonuclease** analysis using BamHI and subsequently by DNA **sequencing** of cloned units. The length variation between short and long units originated from major deletion-insertion events in the noncoding spacer region of the 5S DNA repeat units. In situ **hybridization** with [3H]cRNA and biotin-labelled **probes** synthesized from both the short and long 5S DNA units of S. cereale localized the sites on chromosome 1R and a new site on a chromosome identified as 5R. We propose that the chromosome 1R locus, which has been mapped previously, be named 5SDna-R1 and the second locus, reported in the present paper, be referred to as 5SDna-R2. A preferential **hybridization** of a **probe** from the long unit to the 5SDna-R2 locus and of a **probe** from the short unit to the 5SDna-R1 locus is reported. The clustering of long units in the 5SDna-R2 locus was confirmed by restriction **endonuclease** digestion of DNA from rye chromosome 5R additions to wheat. Nucleotide **sequence** alignment of 5S DNA repeat units from a number of Secale species, using both phenetic and cladistic computer programmes, demonstrated that two clear lineages

corresponding to the long and short units existed in this genus. The different Secale species could not unambiguously differentiated using the 5S DNA **sequences**.

L63 ANSWER 16 OF 27 BIOSIS COPYRIGHT 1995 BIOSIS
AN 89:381210 BIOSIS
DN BA88:61800
TI DISTRIBUTION OF A SECALE-CEREALE DNA REPEAT SEQUENCE AMONG 25 HORDEUM SPECIES.
AU GUPTA P K; FEDAK G; MOLINAR S J; WHEATCROFT R
CS PLANT RES. CENT., AGRIC. CAN., OTTAWA, ONT., CAN. K1A OC6.
SO GENOME 32 (3). 1989. 383-388. CODEN: GENOE3 ISSN: 0831-2796
LA English
AB DNA of 61 accessions representing 25 Hordeum species was tested for homology to a highly repeated 120-bp **sequence** from Secale cereale (rye). Homology to the **probe** (pSC119) was detected in dot blots of all species except H. vulgare (cultivated barley) and its related species, H. agriocrithon and H. spontaneum. **Hybridization** patterns of Southern blots of restriction fragments demonstrated both intraspecific and interspecific variation in the organization of complex units of DNA having homology to the **probe**. For eight species, digestion of the DNA with BamHI gave ladder patterns characteristic of tandem **arrays** of 120-bp repeat units. For EcoRI, HindIII, and SacI digests, the **hybridization** patterns appeared to be highly conserved in the section Hordeum, except those for H. bulbosum, which were unique. A further set of patterns for these three **enzymes** was common among the remaining species of the genus. Thus, DNA **hybridization** with pSC119 generally gave patterns consistent with the current taxonomy of Hordeum species, except that H. bulbosum and H. vulgare were not shown to be closely related.

L63 ANSWER 17 OF 27 BIOSIS COPYRIGHT 1995 BIOSIS DUPLICATE 9
AN 90:155256 BIOSIS
DN BA89:82674
TI VERY LOW RATE Y-CHROMOSOME MOSAICISM 1 5400 DETECTABLE BY A NOVEL **PROBE** ENZYME COMBINATION.
AU NAKAHORI Y; YAMADA M; NAKAGOME Y
CS DEP. CONGENITAL ABNORMALITIES RES., NATL. CHILDREN'S MED. RES. CENTER, SETAGAYA-KU, TOKYO 154, JPN.
SO JPN J HUM GENET 34 (3). 1989. 203-208. CODEN: JIDZA9 ISSN: 0021-5074
LA English
AB DYZ1 is a repetitive DNA family located on the long arm of the Y chromosome and is the major component of the Q-positive region. DYZ1 consists of about 3,000 copies of a 3.4 kb kb repeat unit which mainly consists of a tandem **array** of pentanucleotides, TTCCA. Because of this large number of repeats, DYZ1 hs been used as a **probe** in Southern **hybridization** for sensitive and rapid detection of the Y chromosome. In cases of XX/XY mosaicism, however, autosomal **sequences** having homology to DYZ1 hinder the detection of the Y chromosome, especially when the ratio of the Y-bearing cells is low. To solve this problem and improve the detection limit, we have sought the optimum **hybridization**

condition by changing several variables. These variables include the length of **probes**, the methods of **probe** labeling, the **endonucleases** used to digest the genomic DNA and the hyridization buffer. Here we show that the StuI digestion of genomic DNA in combination with the nick translated DYZ1 **probe** significantly improved the detection limit of the Y-chromosome bearing cells. The presence of Y-chromosome bearing cells was detectable against a background of 5,400-fold female DNA.

L63 ANSWER 18 OF 27 BIOSIS COPYRIGHT 1995 BIOSIS DUPLICATE 10
AN 89:72933 BIOSIS
DN BA87:37331
TI A RELATED MODERATELY REPETITIVE DNA FAMILY IN THE NEMATODES ASCARIS-LUMBRICOIDES AND PANAGRELLUS-SILUSIAE.
AU WARREN T; PASTERNAK J J
CS DEP. BIOL., UNIV. WATERLOO, WATERLOO, ONTARIO N2L 3G1, CANADA.
SO NUCLEIC ACIDS RES 16 (22). 1988. 10833-10848. CODEN: NARHAD ISSN: 0305-1048
LA English
AB Digestion of genomic DNA from the nematodes Panagrellus silusiae and Ascaris lumbricoides with restriction **endonuclease** BamHl releases of 0.7 kilobase (kb) fragment. The 0.7 kb fragment from both nematodes was cloned onto E. coli plasmid pUC19. Using representative clones as DNA **hybridization probes**, it was found that (i) the BamHl fragments cross-**hybridize**; (ii) a ladder-effect with multiples of 0.7 kb was evident in both species after **hybridization** to genomic DNA and (iii) the genomic copy number of BamHl elements is 150 and 195 for P. silusiae and A. lumbricoides respectively. DNA **sequence** analysis of the inserts, AL700-1 and PS700-1, revealed nucleotide blocks with over 85% similarity. No open reading frames are present in either DNA fragment. Neither fragment **hybridizes** to genomic DNA from Caenorhabditis elegans. Northern blot **hybridization** indicated that the 0.7 kb element is transcribed into poly (A)--RNA in P. silusiae; but, is not transcribed in adult Ascaris muscle. Thus, P. silusiae and A. lumbricoides share a homologous, tandemly **arrayed**, moderately repetitive DNA family.

L63 ANSWER 19 OF 27 BIOSIS COPYRIGHT 1995 BIOSIS DUPLICATE 11
AN 86:200566 BIOSIS
DN BA81:91866
TI CLONING AND COMPARISON OF REPEATED DNA SEQUENCES FROM THE HUMAN FILARIAL PARASITE BRUGIA-MALAYI AND THE ANIMAL PARASITE BRUGIA-PAHANGI.
AU MCREYNOLDS L A; DESIMONE S M; WILLIAMS S A
CS NEW ENGLAND BIOLABS, INC., BEVERLY, MASS. 01915.
SO PROC NATL ACAD SCI U S A 83 (3). 1986. 797-801. CODEN: PNASA6 ISSN: 0027-8424
LA English
AB A 320-base-pair repeated **sequence** was observed when DNA samples from the filarial parasites Brugia malayi and Brugia pahangi were digested with the restriction **endonuclease** Hha I. A 640-base-pair dimer of the repeated **sequence** from B. malayi

were inserted into the plasmid pBR322. When dot **hybridization** was used, the copy number of the repeat in B. malayi was found to be about 30,000. The 320-base-pair Hha I repeated **sequences** are arranged in direct tandem **arrays** and comprise about 12% of the genome. B. pahangi has a related repeated **sequence** that cross-**hybridizes** with the cloned B. malayi Hha I repeat. Dot **hybridization** with the clone repeat shows that the **sequence** is present in B. malayi and in B. pahangi but not in four other species of filarial parasites. The cloned repeated DNA **sequence** is an extremely sensitive **probe** for detection of Brugia in blood samples. **Hybridization** with the cloned repeat permits the detection of DNA isolated from a single parasite in an alliquot of blood from animals infected with B. malayi. There are differences in the restriction sites present in the repeated **sequences** that can be used to differentiate between the two Brugia species. The B. malayi repeated DNA **sequence** is cleaved by Alu I and Rsa I but the B. pahangi **sequence** is not. A comparison of repeated **sequences** between the two species by DNA **sequence** analysis indicates that some regions of individual repeats are over 95% homologous, while other short regions are only 60-65% homologous. These differences in DNA **sequence** will allow the construction of species-specific **hybridization probes**.

L63 ANSWER 20 OF 27 BIOSIS COPYRIGHT 1995 BIOSIS DUPLICATE 12
AN 84:330875 BIOSIS
DN BA78:67355
TI ISOLATION OF DNA SEQUENCES PREFERENTIALLY EXPRESSED DURING SPORULATION IN SACCHAROMYCES-CEREVISIAE.
AU PERCIVAL-SMITH A; SEGALL J
CS DEPARTMENT OF BIOCHEMISTRY, UNIVERSITY OF TORONTO, TORONTO, ONTARIO, CANADA M5S 1A8.
SO MOL CELL BIOL 4 (1). 1984. 142-150. CODEN: MCEBD4 ISSN: 0270-7306
LA English
AB A differential **hybridization** screen was used to identify genes cloned from the yeast S. cerevisiae that are expressed preferentially during sporulation. Duplicate copies of a partial Sau3A yeast DNA **library** prepared in the vector pBR322 were **hybridized** with radioactive cDNA [complementary DNA] **probes** representing the mRNA populations of sporulating a.alpha. cells and asporogenous .alpha..alpha. cells at various times after transfer to sporulation medium. Thirty-eight clones showed an enhanced **hybridization** signal with the a.alpha. sporulation **probe** relative to the .alpha..alpha. control cDNA **probe**. A comparison of the **array** of fragments produced by restriction **endonuclease** digestion of these plasmids suggested that 15 different **sequences** had been cloned. An RNA blot analysis using these cloned DNA to **probe** RNA purified from aa, a.alpha. and .alpha..alpha. cells harvested either during vegetative growth or at 10 h after transfer to sporulation medium indicated that 14 different sporulation-specific genes had been identified. Transcripts complementary to these genes are present only in a.alpha. cells after transfer to sporulation

medium. Three of these clones contain 2 sporulation-specific genes. Three genes have been identified that are expressed in all cell types during vegetative growth and only in a.alpha. cells in sporulation medium.

L63 ANSWER 21 OF 27 BIOSIS COPYRIGHT 1995 BIOSIS DUPLICATE 13
AN 84:266587 BIOSIS
DN BA78:3067
TI GENOMIC ORGANIZATION DNA SEQUENCE AND EXPRESSION OF CHICKEN EMBRYONIC HISTONE GENES.
AU SUGARMAN B J; DODGSON J B; ENGEL J D
CS DEP. BIOCHEM., MOL. BIOL. AND CELLBIOL., NORTHWESTERN UNIV., EVANSTON, ILL. 60201.
SO J BIOL CHEM 258 (14). 1983. 9005-9016. CODEN: JBCHA3 ISSN: 0021-9258
LA English
AB The 15 .lambda. Charon 4A recombinant bacteriophage containing histone genes from a chicken genomic **library** were studied. Restriction **enzyme**-mapping analysis and Southern **hybridization** to **sequenced**, homologous histone **probes** indicate that these genes are not tandemly reiterated within the chicken genome; they usually reside in clusters even though there is no unique **array** of genes that appears to constitute a typical cluster. Chicken H4 and H1 genes were identified within the genomic recombinants and subsequently **sequenced** . Extensive regions of homology exist in the 5'- and 3'-flanking regions of the chicken H4 gene when compared to H4 genes from other organisms. In addition to the well documented histone-specific domains, 2 previously unreported regions of homology lie 5' to this gene: an octanucleotide and a pentanucleotide **sequence** lying 59 and 116 nucleotides upstream from the H4 gene CAP site, respectively. The H1 gene **sequence** predicts that the H1 polypeptide is 217 amino acids in length. The 5'-flanking domain of this gene contains, in addition to the transcriptional initiation site and the ATA box, 2 unusual **sequences**: one is a nonamer which resides 29 nucleotides upstream from the ATA box and is conserved in both the chicken and sea urchin H1 genes, while the other is a GC-rich repetitive **sequence** element. The majority of the chicken histone genes among the 15 unique .lambda. recombinant clones are expressed almost exclusively during in ovo development (i.e., from at least 4 days postfertilization up to hatching, about 20-21 days postfertilization) and appear not to be associated with any particular tissue type.

L63 ANSWER 22 OF 27 BIOSIS COPYRIGHT 1995 BIOSIS DUPLICATE 14
AN 83:306925 BIOSIS
DN BA76:64417
TI MOLECULAR CLONING OF COMPLEMENTARY DNA SEQUENCES FOR AVIAN MALIC ENZYME EC-1.1.1.40 NUTRITIONAL AND HORMONAL REGULATION OF MALIC ENZYME MESSENGER RNA LEVELS IN AVIAN LIVER CELLS IN-VIVO AND IN CULTURE.
AU WINBERRY L K; MORRIS S M JR; FISCH J E; GLYNIAS M J; JENIK R A; GOODRIDGE A G
CS DEP. BIOCHEM., CASE WESTERN RESERVE UNIV., CLEVELAND, OHIO 44106.

SO J BIOL CHEM 258 (2). 1983. 1337-1342. CODEN: JBCHA3 ISSN: 0021-9258
LA English
AB A double-stranded cDNA [complementary DNA] **library** constructed from the total poly(A+) RNA of goose uropygial gland was screened for recombinants containing **sequences** complementary to malic **enzyme** mRNA. Replicate **arrays** of 1400 colonies were **hybridized** independently with 32P-labeled cDNA copied from 2 populations of hepatic RNA derived from tissues which differed by about 35-fold with respect to the relative synthesis of malic **enzyme**. Forty-eight of the colonies which gave differential signals were further screened by hybrid-selected translation. DNA from one of these contained an insert of 970 base pairs and selected an mRNA which directed the synthesis of malic **enzyme** in a cell-free system. The malic **enzyme sequences** were subcloned into the single-stranded bacteriophage M13mp8. The subclones were used to prepare 32P-labeled single-stranded **hybridization probe**. Northern analysis indicated that malic **enzyme** mRNA from both goose and chicken is about 2100 bases in length. Hepatic malic **enzyme** mRNA concentration is stimulated 30- to 50-fold or more when neonatal chicks or goslings, respectively, are fed for 24 h. When added to chick embryo hepatocytes in culture, triiodothyronine stimulated malic **enzyme** mRNA accumulation by more than 100-fold. Glucagon inhibited the thyroid hormone-stimulated accumulation of malic **enzyme** mRNA by 99%. In all instances, malic **enzyme** mRNA concentration was closely correlated with the relative rate of malic **enzyme** synthesis. Nutritional and hormonal regulation of malic **enzyme** synthesis probably occurs at the pretranslational level.

L63 ANSWER 23 OF 27 MEDLINE
AN 83143305 MEDLINE
TI Members of the KpnI family of long interspersed repeated sequences join and interrupt alpha-satellite in the monkey genome.
AU Grimaldi G; Singer M F
SO Nucleic Acids Res, (1983 Jan 25) 11 (2) 321-38.
Journal code: O8L. ISSN: 0301-5610.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 8306
AB Three different members of a family (KpnI-family) of interspersed repeated DNA **sequences** were found linked to alpha-satellite **sequences** in cloned segments of the African green monkey genome. In two of these segments the KpnI-family member is over 6 kbp in length and one of them is flanked by alpha-satellite on both sides indicating that it was inserted into a satellite **array**. **Hybridization** of subcloned portions of the family members to restriction **endonuclease** digests of monkey and human DNA and to a genomic **library** of African green monkey DNA indicate that

1) family members are interspersed in both the monkey and human genomes, 2) some family members may include **sequences** in addition to those in the three characterized here, 3) some family members may contain only parts of the **sequences** characterized here and 4) while the overall organization of the family is similar in the human and monkey genome the majority of the family members in each of the two genomes are distinctly identified by the variant position of certain restriction **endonuclease** sites. This last observation suggests that within each genome there is a tendency to maintain particular versions of the **sequence**. Observations 2) and 3) suggest that the KpnI family is complex and includes a variety of subfamilies.

L63 ANSWER 24 OF 27 BIOSIS COPYRIGHT 1995 BIOSIS DUPLICATE 15
AN 83:176037 BIOSIS
DN BA75:26037
TI REPEAT ARRAY IN EPSTEIN BARR VIRUS DNA IS RELATED TO CELL DNA SEQUENCES INTERSPERSED ON HUMAN CHROMOSOMES.
AU HELLER M; HENDERSON A; KIEFF E
CS DEP. MED., LOVLER VIRAL ONCOL. LAB., UNIV. CHICAGO, 910 EAST 58TH STREET, CHICAGO, ILL. 60637.
SO PROC NATL ACAD SCI U S A 79 (19). 1982. 5916-5920. CODEN: PNASA6 ISSN: 0027-8424
LA English
AB The 3rd internal repeat (IR3) simple repeat **array** in Epstein-Barr virus (EBV) DNA has a high degree of homology to a reiterated component of cell DNA. 32P-Labeled human or mouse DNA **hybridize** to the IR3 **sequence** on Southern blots of viral DNA. EBV IR3 **probe** identifies many restriction **enzyme** fragments on Southern blots of human and mouse DNA that have extensive homology to IR3. Cytological **hybridization** shows that IR3 is homologous to at least 1 region on each human chromosome except the Y chromosome.

L63 ANSWER 25 OF 27 BIOSIS COPYRIGHT 1995 BIOSIS DUPLICATE 16
AN 80:193699 BIOSIS
DN BA69:68695
TI ORGANIZATION OF REPEATED REGIONS WITHIN THE EPSTEIN BARR VIRUS DNA MOLECULE.
AU HAYWARD S D; NOGEE L; HAYWARD G S
CS DEP. PHARMACOL. EXP. THER., JOHNS HOPKINS UNIV. SCH. MED., BALTIMORE, MD. 21205, USA.
SO J VIROL 33 (1). 1980. 507-521. CODEN: JOVIAM ISSN: 0022-538X
LA English
AB Virions of human Epstein-Barr virus released from the B95-8 line of marmoset lymphoblasts have linear double-stranded DNA molecules of 115 .times. 106 MW (180 .+-. 10 kilobase [kb] pairs). Approximately 20% of this DNA yields multiple fragments of 3200 base pairs when cleaved with BglII, BamHI, PvuII, SacI, SstII or XhoI restriction **enzymes**. The results of cleavage site mapping with these and other **enzymes**, together with blot **hybridization** experiments using the 3.2 kb pair BglII-R fragment as a **probe** , indicate that these fragments originate from an internal region

between 0.710-0.915 map units containing a cluster of at least 12 apparently identical repetitions of a **sequence** with relatively high guanine plus cytosine content. The repeat units are arranged in adjacent tandem **array** with all copies having the same orientations and they form a series of oligomers of tailed double-stranded circles when fragments containing portions of the cluster are denatured and reannealed. Physical maps of cleavage sites within the 3.2 kb pair repeat units and in the flanking **sequences** surrounding the repeat cluster were constructed. The Epstein-Barr virus DNA molecule, like those of other mammalian herpesviruses, is divisible into a large L segment and a smaller S segment. The detailed arrangement of repetitive **sequences** within the Epstein-Barr virus S segment differs significantly from that in all other herpesvirus genomes described so far.

L63 ANSWER 26 OF 27 BIOSIS COPYRIGHT 1995 BIOSIS DUPLICATE 17
AN 79:259246 BIOSIS
DN BA68:61750
TI CONSERVATION OF REPEATED DNA SEQUENCES IN ANEU PLOID HUMAN TUMOR CELLS.
AU MANUELIDIS L; MANUELIDIS E E
CS DEP. PATHOL., YALE UNIV. SCH. MED., 310 CEDAR ST., NEW HAVEN, CONN. 06510, USA.
SO CHROMOSOMA (BERL) 72 (3). 1979. 257-270. CODEN: CHROAU ISSN: 0009-5915
LA English
AB A series of human neuroectodermal tumors, all containing more than the normal diploid DNA, and each with its own distinct chromosome mode, were studied using restriction **enzyme** cleavage and specific DNA **sequence hybridization**. Methods described were quite sensitive and quantitative and as few as 40 molecules with a given restriction site were reproducibly detected in total nuclear DNA. Analysis of several fluorescent gel bands associated with different chromosomal domains revealed no changes between any of the tumor and normal cells. Specific **probe hybridization**, using purified complex repeating **sequences**, indicated fidelity of base **sequence**, as well as preservation of the relative amounts of each of a number of minor related multimers in both the tumor and normal cells. Centromeric regions containing **arrays** of such **sequences** may be maintained in these tumor cells. Some of these cells may be polyploid with respect to DNA **sequences**, rather than aneuploid as their chromosome profiles suggest.

L63 ANSWER 27 OF 27 BIOSIS COPYRIGHT 1995 BIOSIS
AN 77:222488 BIOSIS
DN BA64:44852
TI CLONING AND CHARACTERIZATION OF A COMPLEX SATELLITE DNA FROM DROSOPHILA-MELANOGASTER.
AU CARLSON M; BRUTLAG D
SO CELL 11 (2). 1977 371-382. CODEN: CELLB5 ISSN: 0092-8674
LA Unavailable
AB The **sequence** organization of the 1.688 satellite DNA

(density 1.688 g/cm3 in CsCl) were investigated, and this satellite differed from the other D. melanogaster satellite DNA in having a much greater **sequence** complexity. Purification of 1.688 satellite DNA by successive equilibrium density centrifugations yielded a fraction 77% pure. Segments of satellite DNA were isolated by molecular cloning in the plasmid vector pSC101. One recombinant plasmid contained a segment of 1.688 satellite DNA 5.8 kilobase pairs in size and was stable during propagation in Escherichia coli. Recognition sites for restriction **enzymes** from Haemophilus aegyptius (Hae III), H. influenzae f (Hinf) and Arthrobacter luteus (Alu I) were mapped in the satellite DNA of this hybrid plasmid. The spacing of Hae III, Hinf and 2 Alu I sites at regular intervals of about 365 base pairs is strong evidence that the **sequence** complexity of this satellite DNA is 365 base pairs. Further evidence comes from the finding that both gradient-purified and cloned 1.688 satellite DNA renature with their Hae II sites in register. The Hae III and Hinf sites in gradient-purified satellite DNA were shown by others to be distributed at intervals of 365 base pairs and integral multiples thereof. Some of the sites in an otherwise regular **array** were randomly inactivated. Cloned satellite DNA provided a **hybridization probe** for sensitive studies of the arrangement of these recognition sites in gradient-purified satellite DNA. Some regions of satellite DNA contained many fewer recognition sites than expected from the proposed models. Different regions of 1.688 satellite DNA may exhibit different arrangements of Hae III and Hinf recognition sites.